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Reviewer: markspencer

Timestamp: [year=2008; month=11; day=24; hr=11; min=2; sec=3; ms=38;]

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Application No: 10559994 Version No: 1.0

Input Set:

Output Set:

Started: 2008-10-31 15:30:10.087

Finished: 2008-10-31 15:30:10.704

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 617 ms

Total Warnings: 4

Total Errors: 0

No. of SeqIDs Defined: 4

Actual SeqID Count: 4

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SEQUENCE LISTING

<110> Thompson, Timothy C
Ren, Chenghui
Ren, Chengzhen

<120> RTVP-GLIPR-LIKE COMPOSITIONS AND METHODS FOR THE DETECTION,
TREATMENT AND PREVENTION OF PROSTATE CANCER

<130> PRO025/4-012US

<140> 10559994

<141> 2008-10-31

<150> 60/477130

<151> 2003-06-09

<150> PCT/US04/18731

<151> 2004-06-08

<160> 4

<170> PatentIn version 3.5

<210> 1

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<212> DNA

<213> Homosapiens

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<221> CDS

<222> (28)..(726)

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Leu Trp Ile Leu Gly Leu Cys Leu Val Ala Thr Thr Ser Ser Lys Ile
10               15               20               25
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cca tcc atc act gac cca cac ttt ata gac aac tgc ata gaa gcc cac      150
Pro Ser Ile Thr Asp Pro His Phe Ile Asp Asn Cys Ile Glu Ala His
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Asn Glu Trp Arg Gly Lys Val Asn Pro Pro Ala Ala Asp Met Lys Tyr
               45               50               55
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atg att tgg gat aaa ggt tta gca aag atg gct aaa gca tgg gca aac      246
Met Ile Trp Asp Lys Gly Leu Ala Lys Met Ala Lys Ala Trp Ala Asn
               60               65               70
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cag tgc aaa ttt gaa cat aat gac tgt ttg gat aaa tca tat aaa tgc      294
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[illegible]

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Phe Ile Asp Asn Cys Ile Glu Ala His Asn Glu Trp Arg Gly Lys Val
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Asn Pro Pro Ala Ala Asp Met Lys Tyr Met Ile Trp Asp Lys Gly Leu
50 55 60

Ala Lys Met Ala Lys Ala Trp Ala Asn Gln Cys Lys Phe Glu His Asn
65 70 75 80

Asp Cys Leu Asp Lys Ser Tyr Lys Cys Tyr Ala Ala Phe Glu Tyr Val
85 90 95

Gly Glu Asn Ile Trp Leu Gly Gly Ile Lys Ser Phe Thr Pro Arg His
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Ala Ile Thr Ala Trp Tyr Asn Glu Thr Gln Phe Tyr Asp Phe Asp Ser
115 120 125

Leu Ser Cys Ser Arg Val Cys Gly His Tyr Thr Gln Leu Val Trp Ala
130 135 140

Asn Ser Phe Tyr Ala Gly Cys Ala Val Ala Met Cys Pro Asn Leu Gly
145 150 155 160

Gly Ala Ser Thr Ala Ile Phe Val Cys Asn Tyr Gly Pro Ala Gly Asn
165 170 175

Phe Ala Asn Met Pro Pro Tyr Val Arg Gly Glu Ser Cys Ser Leu Cys
180 185 190

Pro Lys Glu Glu Lys Cys Val Lys Asn Leu Cys Lys Asn Pro Phe Leu
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Leu Gly Phe Leu Leu Leu Arg Ile Phe
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Leu Trp Ile Leu Gly Leu Cys Leu Val Ala Thr Thr Ser Ser Lys Ile
10 15 20 25

cca tcc atc act gac cca cac ttt ata gac aac tgc ata gaa gcc cac 150
Pro Ser Ile Thr Asp Pro His Phe Ile Asp Asn Cys Ile Glu Ala His
30 35 40

aac gaa tgg cgt ggc aaa gtc aac cct ccc gcg gcc gac atg aaa tac 198
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45 50 55

atg att tgg gat aaa ggt tta gca cag atg gct aaa gca tgg gca aac 246
Met Ile Trp Asp Lys Gly Leu Ala Gln Met Ala Lys Ala Trp Ala Asn
60 65 70

cag tgc aaa ttt gaa cat aat gac tgt ttg gat aaa tca tat aaa tgc 294
Gln Cys Lys Phe Glu His Asn Asp Cys Leu Asp Lys Ser Tyr Lys Cys
75 80 85

tat gca gct ttt gaa tat gtt gga gaa aat atc tgg tta ggt gga ata 342
Tyr Ala Ala Phe Glu Tyr Val Gly Glu Asn Ile Trp Leu Gly Gly Ile
90 95 100 105

aag tca ttc aca cca aga cat gcc att acg gct tgg tat aat gaa acc 390
Lys Ser Phe Thr Pro Arg His Ala Ile Thr Ala Trp Tyr Asn Glu Thr
110 115 120

caa ttt tat gat ttt gat agt cta tca tgc tcc aga gtc tgt ggc cat 438
Gln Phe Tyr Asp Phe Asp Ser Leu Ser Cys Ser Arg Val Cys Gly His
125 130 135

tat aca cag tta gtt tgg gcc aat tca ttt tat gtc ggt tgt gca gtt 486
Tyr Thr Gln Leu Val Trp Ala Asn Ser Phe Tyr Val Gly Cys Ala Val
140 145 150

gca atg tgt cct aac ctt ggg gga gct tca act gca ata ttt gta tgc 534
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155 160 165

aac tac gga cct gca gga aat ttt gca aat atg cct cct tac gta aga 582
Asn Tyr Gly Pro Ala Gly Asn Phe Ala Asn Met Pro Pro Tyr Val Arg
170 175 180 185

gga gaa tct tgc tct ctc tgc tca aaa gaa gag aaa tgt gta aag aac	630
Gly Glu Ser Cys Ser Leu Cys Ser Lys Glu Glu Lys Cys Val Lys Asn	
190 195 200	

ctc tgc agg act cca caa ctt att ata cct aac caa aat cca ttt ctg	678
Leu Cys Arg Thr Pro Gln Leu Ile Ile Pro Asn Gln Asn Pro Phe Leu	
205 210 215	

aag cca acg ggg aga gca cct cag cag aca gcc ttt aat cca ttc agc	726
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220 225 230	

tta ggt ttt ctt ctt ctg aga atc ttt taatgtcatt tatatacaaa	773
Leu Gly Phe Leu Leu Leu Arg Ile Phe	
235 240	

agaaattctc aaatgttaaa ataaaggaat agtttattgc ttaatataac ttatcatcac	833
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20 25 30

Phe Ile Asp Asn Cys Ile Glu Ala His Asn Glu Trp Arg Gly Lys Val
35 40 45

Asn Pro Pro Ala Ala Asp Met Lys Tyr Met Ile Trp Asp Lys Gly Leu
50 55 60

Ala Gln Met Ala Lys Ala Trp Ala Asn Gln Cys Lys Phe Glu His Asn
65 70 75 80

Asp Cys Leu Asp Lys Ser Tyr Lys Cys Tyr Ala Ala Phe Glu Tyr Val
85 90 95

Gly Glu Asn Ile Trp Leu Gly Gly Ile Lys Ser Phe Thr Pro Arg His
100 105 110

Ala Ile Thr Ala Trp Tyr Asn Glu Thr Gln Phe Tyr Asp Phe Asp Ser
115 120 125

Leu Ser Cys Ser Arg Val Cys Gly His Tyr Thr Gln Leu Val Trp Ala
130 135 140

Asn Ser Phe Tyr Val Gly Cys Ala Val Ala Met Cys Pro Asn Leu Gly
145 150 155 160

Gly Ala Ser Thr Ala Ile Phe Val Cys Asn Tyr Gly Pro Ala Gly Asn
165 170 175

Phe Ala Asn Met Pro Pro Tyr Val Arg Gly Glu Ser Cys Ser Leu Cys
180 185 190

Ser Lys Glu Glu Lys Cys Val Lys Asn Leu Cys Arg Thr Pro Gln Leu
195 200 205

Ile Ile Pro Asn Gln Asn Pro Phe Leu Lys Pro Thr Gly Arg Ala Pro
210 215 220

Gln Gln Thr Ala Phe Asn Pro Phe Ser Leu Gly Phe Leu Leu Leu Arg
225 230 235 240

Ile Phe